

~~Testis Clave~~

HZCYTOR02.SEQ - [redacted]  
Sequence of pcr products generated with 9800-9802,  
nested pcr product 9941-AP2 (9801-AP1)  
nested pcr product 9937-AP2 (9803-AP1)

Enzyme	Recognition	Cut Site
AgeI	(A <sup>^</sup> CCGGT)	Def: 1124
BamHI	(G <sup>^</sup> GATCC)	Def: 172
DraI	(TTT <sup>^</sup> AAA)	Def: 36
EcoRI	(G <sup>^</sup> AATTC)	Def: 450
EcoRV	(GAT <sup>^</sup> ATC)	Def: 438
HpaI	(GTT <sup>^</sup> AAC)	Def: 145
MscI	(TGG <sup>^</sup> CCA)	Def: 1244
MunI	(C <sup>^</sup> AATTG)	Def: 493
NcoI	(C <sup>^</sup> CATGG)	Def: 377
NsiI	(ATGCA <sup>^</sup> T)	Def: 592
Ppu10I	(A <sup>^</sup> TGCAT)	Def: 588
SmaI	(CCC <sup>^</sup> GGG)	Def: 11
SspI	(AAT <sup>^</sup> ATT)	Def: 503 988 1107
XmaI	(C <sup>^</sup> CCGGG)	Def: 9

This should be the full  
sequence. The other  
sequence I gave you had  
3 mistakes in it.

[redacted]

HZCYTOR02.SEQ Linear LENGTH = 1289

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      XmaI      SmaI      DraI      49
      |         |         |
1  CCCCCCGCCGGGAGAGAGGCAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTGGCT 69
   GGGGGGCGGCGCTCTCTCCGTTATAGTTCCAAAATTTAGAGCCTCTTACCGAAAGCAAACGAACCGA
      11         36         M A F V C L A 7
9

70 ATCGGATGCTTATATACCTTTCTGATAAGCACAACTTTGGCTGTACTTTCATCTTCAGACACCGAGATA 138
   TAGCCTACGAATATATGGAAAGACTATTCGTGTTGTAACCGACATGAAGTAGAAGTCTGGCTCTAT
   I G C L Y T F L I S T T F G C T S L S D T E I 30
                                   Prd. N-term 525

      HpaI      BamHI
      |         |
139 AAAGTTAACCCTCCTCAGGATTTGAGATAGTGGATCCCGGATACTTAGGTTATCTCTATTGCAATGG 207
    TTTCAATTGGGAGGAGTCTCTAAACTCTATCACCTAGGGCCTATGAATCCAATAGAGATAAACGTTACC
    K V N P P Q D F E I V D P G Y L G Y L Y L Q W 53
      145         172

208 CAACCCCCACTGTCTCTGGATCATTTAAGGAATGCACAGTGAATATGAACTAAAATACCGAAACATT 276
    GTTGGGGGTGACAGAGACCTAGTAAAATCTCTACGTGTACCTTATACCTGATTATGCTTTGTAA
    Q P P L S L D H F K E C T V E Y E L K Y R N I 76

277 GGTAGTGAAACATGGAAGACCATCATTACTAAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAG 345
    CCATCACTTTGTACCTTCTGGTAGTAATGATTCTTAGATGTAATGTTTCTACCCAAACTAGAATTGTT
    G S E T W K T I I T K N L H Y K D G F D L N K 99

      NcoI
      |
346 GGCATTGAAGCGAAGATACACACGCTTTTACCATTGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCC 414
    CCGTAACCTTCGCTTCTATGTGTGCGAAAATGGTACCGTTACGTGTTACCTAGTCTTCAAGTTTCAAG
    G I E A K I H T L L P W Q C T N G S E V Q S S 122
      377

      EcoRV      EcoRI
      |         |
415 TGGGCAGAACTACTTATTGGATATCACCACAAGGAATTCAGAACTAAAGTTCAGGATATGGATTGC 483
    ACCCGTCTTTGATGAATAACCTATAGTGGTGTCTTAAAGGTCTTTGATTCAAGTCTATACCTAACG
    W A E T T Y W I S P Q G I P E T K V Q D M D C 145
      438         450

      MunI      SspI
      |         |
484 GTATATTACAATTGGCAATATTTACTCTGTTCTTGAAACCTGGCATAGGTGTACTTCTTGATACCAAT 552
    CATATAATGTTAACCGTTATAAATGAGACAAGAACCTTTGGACCGTATCCACATGAAGAACTATGGTTA
    V Y Y N W Q Y L L C S W K P G I G V L L D T N 168
      493         503
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23 a.a / line

maximize 25-380  
Prd = 25  
EK-cell - 25-339  
Prd 340-363  
Cyto 364-380

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[redacted]

Ppu101  
NsiI

553 TACAACCTGTTTACTGGTATGAGGGCTTGGATCATGCATTACAGTGTGTTGATTACATCAAGGCTGAT 621  
ATGTTGAACAAAATGACCATACTCCCGAACCTAGTACGTAATGTACACAACTAATGTAGTCCGACTA  
Y N L F Y W Y E G L D H A L Q C V D Y I K A D 191  
592  
588

622 GGACAAAATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATAAAGATTTCTATTTGTGTT 690  
CCTGTTTATATCCTACGTCTAAAGGGATAAACCTCCGTAGTCTGATATTTCTAAAGATATAACACAA  
G Q N I G C R F P Y L E A S D Y K D F Y I C V 214

691 AATGGATCATCAGAGAACAAGCCTATCAGATCCAGTATTTTCACTTTTCAGCTTCAAAATATAGTTAAA 759  
TTACCTAGTAGTCTCTTGTTCGGATAGTCTAGGTCAATAAAGTGAAAGTCGAAGTTTATATCAATTT  
N G S S E N K P I R S S Y F T E Q L Q N I V K 237

760 CCTTTGCCGCCAGTCTATCTTACTTTTACTCGGGAGAGTTTATGTGAAATTAAGCTGAAATGGAGCATA 828  
GGAAACGGCGGTCAGATAGAATGAGCCCTCTCAAGTACACTTTAATTCGACTTTACGTCGTAT  
P L P P V Y L T F T R E S S C E I K L K W S I 260

829 CCTTTGGGACCTATTCAGCAAGGTGTTTTGATTATGAAATTGAGATCAGAGAAGATGATACTACCTTG 897  
GGAAACCCCTGGATAAGGTCGTTCCACAAAATACTTTAACTCTAGTCTCTTCTACTATGATGGAAC  
P L G P I P A R C F D Y E I E I R E D D T T L 283

898 GTGACTGCTACAGTTGAAAATGAAACATACACCTTGAAAACAACAAATGAAACCCGACAATTATGCTTT 966  
CACTGACGATGTCAACTTTTACTTTGTATGTGGAACCTTTGTTGTTTACTTTGGGCTGTTAATACGAAA  
V T A T V E N E T Y T L K T T N E T R Q L C F 306

SspI

967 GTAGTAAGAAGCAAAGTGAATATTTATTGCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATAAACAA 1035  
CATCATTTCTTCGTTTCACTTATAAATAACGAGTCTACTGCCTTAAACCTCACTCACCTCACTATTTGTT  
V V R S K V N I Y C S D D G I W S E W S D K Q 329  
988

1036 TGCTGGGAAGGTGAAGACCTATCGAAGAAAACCTTTGCTACGTTTCTGGCTACCATTTGGTTTCATCTTA 1104  
ACGACCCCTTCCACTTCTGGATAGCTTCTTTTGAACGATGCAAGACCGATGGTAAACCAAAGTAGAAT  
C W E G E D L S K K T L L R F W L P F G F I L 352  
337 TMD

SspI

AgeI

1105 ATATTAGTTATATTTGTAACCGGTCTGCTTTTGGCTAAGCCAAACACCTACCCAAAAATGATTCCAGAA 1173  
TATAATCAATATAAACATTGGCCAGACGAAAACGCATTTCGGTTTGTGGATGGGTTTTACTAAGGTCTT  
I L V I F V T G L L L R K P N T Y P K M I P E 375  
1107 1124 363

1174 TTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATG 1242  
AAAAAGACACTATGTACTTCTGAAAGGTATAGTTCTCTGTACCATAACTGAGTTGTCAAAGGTCAGTAC  
F F C D T .

MscI

1243 GCCAAATGTTCAATATGAGTCTCAATAAACTGAATTTTCTTGGCAA 1289  
CGGTTTACAAGTTATACTCAGAGTTATTTGACTTAAAAAGAACGCTT  
1244

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